

8'3046

STIC-Biotech/ChemLib

From: Bunner, Bridget
Sent: Thursday, January 23, 2003 2:33 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like a sequence search performed for case 09/893,348:

1. the amino acid sequence of SEQ ID NO: 19

Thanks!

Bridget Bunner

Art Unit 1647
CM1-10D12
(703) 305-7148
mailbox 10B19

WIFE

POINT OF CONTACT:
PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
CORPORATE (703) 305-1954

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 1/24
Date Completed: 1/24
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



GenCore version 5.1.3
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protein - protein search, using sw model

on: January 24, 2003, 11:08:03 ; Search time 35 Seconds
(without alignments)
68.529 Million cell updates/sec

US-09-893-348-19
1 SYDSIKLEPPNPPPYEFA 18

BLASTSUM62
Gap 10 0, 14px 0 5

arched: 908470 seqs, 133250620 residues

al number of hits satisfying chosen parameters: 908470

imum DB seq length: 0
imum BP seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- A Geneseq 101002:*
- 1: /SID32/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
 - 2: /SID32/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
 - 3: /SID32/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
 - 4: /SID32/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
 - 5: /SID32/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
 - 6: /SID32/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
 - 7: /SID32/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
 - 8: /SID32/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
 - 9: /SID32/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
 - 10: /SID32/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
 - 11: /SID32/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
 - 12: /SID32/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
 - 13: /SID32/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
 - 14: /SID32/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
 - 15: /SID32/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
 - 16: /SID32/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
 - 17: /SID32/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
 - 18: /SID32/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
 - 19: /SID32/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
 - 20: /SID32/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
 - 21: /SID32/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
 - 22: /SID32/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
 - 23: /SID32/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	99	100.0	18	21	AAV71335
2	99	100.0	191	21	AAV71400
3	99	100.0	356	21	AAV71390
4	99	100.0	374	21	AAV71397
5	99	100.0	475	21	AAV71389
6	99	100.0	502	21	AAV71396
7	99	100.0	552	21	AAV71388
8	99	100.0	684	21	AAV71394
9	99	100.0	695	21	AAV71387
10	99	100.0	732	21	AAV71399

11	99	100.0	736	21	AAV71398	Pat Nogo A protein
12	99	100.0	737	21	AAV71386	Rat Nogo A protein
13	99	100.0	746	21	AAV71391	Rat Nogo A protein
14	99	100.0	803	21	AAV71362	Rat Nogo A protein
15	99	100.0	974	21	AAV71560	Rat Nogo A protein
16	99	100.0	1162	21	AAV71557	Pat Nogo A protein
17	99	100.0	1163	21	AAV71310	Pat Nogo A protein
18	99	100.0	1163	21	AAV71384	Alternative version
19	99	100.0	1163	21	AAV71384	Human secreted pro
20	85	85.9	642	19	AAV58383	Human secreted pro
21	85	85.9	642	22	AAV58062	Human secreted pro
22	85	85.9	642	22	AAV58012	Human secreted pro
23	85	85.9	1178	21	AAV71311	Human neurite grow
24	85	85.9	1192	21	AAV56967	Human MAFI polypep
25	85	85.9	1192	21	AAV56967	Human MAFI polypep
26	85	85.9	1192	21	AAV56967	Human MAFI polypep
27	85	85.9	1192	21	AAV56967	Human MAFI polypep
28	85	85.9	1192	21	AAV56967	Human MAFI polypep
29	85	85.9	1192	21	AAV56967	Human MAFI polypep
30	85	85.9	1192	21	AAV56967	Human MAFI polypep
31	85	85.9	1192	21	AAV56967	Human MAFI polypep
32	85	85.9	1192	21	AAV56967	Human MAFI polypep
33	85	85.9	1192	21	AAV56967	Human MAFI polypep
34	85	85.9	1192	21	AAV56967	Human MAFI polypep
35	85	85.9	1192	21	AAV56967	Human MAFI polypep
36	85	85.9	1192	21	AAV56967	Human MAFI polypep
37	85	85.9	1192	21	AAV56967	Human MAFI polypep
38	85	85.9	1192	21	AAV56967	Human MAFI polypep
39	85	85.9	1192	21	AAV56967	Human MAFI polypep
40	85	85.9	1192	21	AAV56967	Human MAFI polypep
41	85	85.9	1192	21	AAV56967	Human MAFI polypep
42	85	85.9	1192	21	AAV56967	Human MAFI polypep
43	85	85.9	1192	21	AAV56967	Human MAFI polypep
44	85	85.9	1192	21	AAV56967	Human MAFI polypep
45	85	85.9	1192	21	AAV56967	Human MAFI polypep

ALIGNMENTS

RESULT 1	AAV71335	standard; peptide; 18 AA.
XX	AAV71335;	
XX	02-NOV-2000	(first entry)
DE	Bovine P472 peptide for antisera production	
XX	Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;	
KW	central nervous system; neoplastic disease; antiproliferative; glioma;	
KW	antigenic gene therapy; neuroblastoma; menigioma; retinoblastoma;	
KW	degenerative nerve disease; Alzheimer's disease; Parkinson's disease;	
KW	hyperproliferative disorder; benign dysproliferative disorder; diagnosis;	
KW	proliferative; tissue hypertrophy; neuronal regeneration; treatment;	
KW	structural plasticity; screening; P472 peptide; AS 472; antiserum.	
OS	Bos sp.	
XX	WO2000031235-A2.	
PN	02-JUN-2000.	
XX	05-NOV-1999.	99WO-US26160.
XX	06-NOV-1998.	98US-0107446.
PR	(SCHW/) SCHWAB M E.	
XX	(CHEN/) CHEN M S.	
PA	Schwab ME, Chen MS;	
PI		
XX		

Rattus sp.
 WO200031235-A2.
 02-JUN-2000.
 05-NOV-1999; 99WO-US26160.
 06-NOV-1999; 98US-0107446.
 (SCHWAB M E.
 (CHEN M S.
 Schwab ME, Chen MS;
 WPI: 2000-400052/34.
 Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons -

Example; Page : 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAY71310, which is used in the construction of mutant NiG-D5. NiG-D5 is composed of His-tag/77-tag/Nogo-A sequence aa 291-646/His-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading.
 Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 356 AA;

Query Match 100.0%; Score 99; DB 21; Length 356;

Best Local Similarity 100.0%; Pred No 2,7e-06; Mismatches 0; Gaps 0;

Matches 18; Conservative 0; Indels 0; Gaps 0;
 1 SYDSIKLEPPNPPPEEA 18
 |||
 333 SYDSIKLEPPNPPPEEA 350

SVSUT 4

AAV71397 standard; Protein; 374 AA.

AAV71397;

02 NOV-2000 (first entry)

DE Rat Nogo A protein fragment used in the construction of mutant NiG-D16.
 XX
 XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; muten.
 XX
 XX Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 1..18
 FT /note= "Corresponds to residues 172-189 of Nogo A
 FT sequence shown in AAY71310"
 FT Region 19..374
 FT /note= "Corresponds to residues 619-974 of Nogo A
 FT sequence shown in AAY71310"
 XX
 XX WO200031235 A2.
 XX
 XX 02-JUN-2000.
 XX
 XX 05-NOV-1999; 99WO-US26160.
 XX
 XX 06-NOV-1999; 98US-0107446.
 XX
 XX (SCHWAB M E.
 XX (CHEN M S.
 XX Schwab ME, Chen MS;
 XX WPI: 2000-400052/34.
 XX
 XX Nogo proteins and nucleic acids useful for treating neoplastic
 PT disorders of the central nervous system and inducing regeneration of
 PT neurons -
 XX
 XX Example; Page : 122pp; English.

XX The patent relates to neurite growth inhibitor Nogo which is free of
 CC all central nervous system (CNS) myelin material with which it is
 CC naturally associated. Nogo proteins and fragments displaying neurite
 CC growth inhibitory activity are used in the treatment of neoplastic
 CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
 CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
 CC neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma
 CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
 CC diseases. Therapeutics which promote Nogo activity can be used to treat
 CC or prevent hyperproliferative or benign dysproliferative disorders e.g.
 CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
 CC acids can be used to inhibit production of Nogo protein to induce
 CC regeneration of neurons or to promote structural plasticity of the CNS
 CC in disorders where neurite growth, regeneration or maintenance are
 CC deficient or desired. The animal models can be used in diagnostic and
 CC screening methods for predisposition to disorders and to screen for or
 CC test molecules which can treat or prevent disorders or diseases of the
 CC CNS. The present sequence is derived by fusing two fragments of rat Nogo
 CC A protein shown in AAY71310, which is used in the construction of mutant
 CC NiG-D16. NiG-D16 is composed of
 CC His-tag/77-tag/Nogo-A sequence aa 172-189 + 619-974/His-tag.
 CC Nogo A deletion mutants were used for mapping the inhibitory
 CC sites of Nogo protein. Major inhibitory region was identified in the
 CC Nogo A sequence from amino acids 172-974, particularly amino acids
 CC 542-722. In addition, N-terminal region 1-171 was found to be inhibitory
 CC to NIH 3T3 fibroblast spreading.
 CC Note: The present sequence is not given in the specification but is
 CC derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42
 CC are referred in claim 32 and SEQ ID NO: 29 in disclosure of the
 CC specification. However, the specification does not include sequences for
 CC these SEQ ID numbers.
 XX

Sequence: 374 AA;
Query Match: 100.0%, Score: 39, DB: 21, Length: 374,
Best Local Similarity: 100.0%, Pred. No.: 2,000,000,
Matches: 14, Conservative: 2, Mismatches: 0, Indels: 0, Gaps: 0,
1 SYDSIKLEPENPPYEAA 19
|||||
23 SYDSIKLEPENPPYEAA 40

Query Match: 100.0%, Score: 39, DB: 21, Length: 374,
Best Local Similarity: 100.0%, Pred. No.: 2,000,000,
Matches: 14, Conservative: 2, Mismatches: 0, Indels: 0, Gaps: 0,
1 SYDSIKLEPENPPYEAA 19
|||||
23 SYDSIKLEPENPPYEAA 40

AAV71396
02 NOV 2000 (first entry)
Rat Nogo A protein fragment used in the construction of mutant NIG-D4.

Rat: neurite growth inhibitor; Nogo A, neural cell, myelin, CNS;
central nervous system; neoplastic disease; antiproliferative; glioma;
antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
hypertrophic tissue hypertrophy; benign dysproliferative disorder; diagnosis;
proliferative tissue hypertrophy; neuronal regeneration; treatment;
structural plasticity; screening; mutant; mutagen.

Rattus sp.
W0200031235 AA;
02 JUN 2000.
05 NOV 1999; 99NW-US26160.
06 NOV 1998; 98US-0107446.
(SCHW/) SCHWAB M E.
(CHEN/) CHEN M S.
Schwab ME, Chen MS;
WPI: 2000 400052/34.
Note: proteins and nucleic acids useful for treating neoplastic
disorders of the central nervous system and inducing regeneration of
neurons

Example: Page: 122pf; English.
The patent relates to neurite growth inhibitor Nogo which is free of
all central nervous system (CNS) myelin material with which it is
natively associated. Nogo proteins and fragments displaying neurite
growth inhibitory activity are used in the treatment of neoplastic
disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
craniopharyngioma, ependymoma, fibrosarcoma, haemangioblastoma, acoustic
neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma
and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
disease. Therapies which promote neuro activity can be used to treat
or prevent hypofunction of a benign dysproliferative disorder e.g.
neuroblastoma and tissue hypertrophy. Fibrosarcoma or antisense Nogo nucleic
acids can be used to inhibit production of Nogo protein to induce
regeneration of neurons or to promote structural plasticity of the CNS
in disorders where neurite growth, regeneration or maintenance are
deficient or desired. The animal models can be used in diagnostic and
screening methods for predisposition to disorders and to screen for or
test molecules which can treat or prevent disorders or diseases of the
CNS. The present sequence is a fragment of rat Nogo A protein shown in
AAV71396, which is used in the construction of mutant NIG-D4. NIG-D4
is composed of His 14779-14793. A sequence as 122.646/vector
Nogo A deletion mutants were used for mapping the inhibitory sites of

CC Nogo protein. Major inhibitory region was identified in the
CC Nogo A sequence from amino acids 172-974, particularly amino acids
CC 543-723. In addition, N-terminal region 1-101 was found to be inhibitory
CC to NIH 3T3 fibroblast spreading.
CC Note: The present sequence is not given in the specification but is
CC derived from rat Nogo A sequence shown in AAV71396. SEQ ID numbers 35-42
CC are referred to in claim 31 and SEQ ID No. 39 is designated as the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers.
XX
SQ Sequence 475 AA;
Query Match: 100.0%; Score: 99; DB: 21; Length: 475;
Best Local Similarity: 100.0%; Pred. No.: 3,700,000;
Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 1 SYDSIKLEPENPPYEAA 18
|||||
Db 452 SYDSIKLEPENPPYEAA 469

RESULT 6
AAV71396
ID AAV71396 standard, Protein, 502 AA.
XX
AC AAV71396,
XX
DT 02 NOV 2000 (first entry)
XX
DE Rat Nogo A protein fragment used in the construction of mutant NIG-D4.
XX
XX Rat: neurite growth inhibitor; Nogo A, neural cell, myelin, CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hypertrophic tissue hypertrophy; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening; mutant; mutagen.
XX
OS Rattus sp.
XX
XX
XX Key Location/Qualifiers
XX FH 1..18
XX FT Region /note="Corresponds to residues 172-189 of Nogo A
XX FT sequence shown in AAV71310"
XX FT Region 19..502
XX FT /note="Corresponds to residues 491-504 of Nogo A
XX FT sequence shown in AAV71310"
XX
XX W0200031235 AA.
XX PN
XX PD 02 JUN 2000.
XX
XX 05 NOV 1999; 99NW-US26160
XX PP 06 NOV 1998; 98US-0107446.
XX PA (SCHW/) SCHWAB M E.
XX PA (CHEN/) CHEN M S.
XX PI Schwab ME, Chen MS;
XX PP WPI: 2000 400052/34.
XX DP
XX PT Nogo proteins and nucleic acids useful for treating neoplastic
XX disorders of the central nervous system and inducing regeneration of
XX neurons -
XX
XX Example: Page: 122pf; English.
XX
XX The patent relates to neurite growth inhibitor Nogo which is free of
XX all central nervous system (CNS) myelin material with which it is
XX natively associated. Nogo proteins and fragments displaying neurite

Growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma diseases. Therapeutic which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments of the Nogo A protein shown in AAY71310, which is used in the construction of mutant Nig-D15. Nig-D15 is composed of His-tag/77-cag/Nogo-A sequence aa 172-189 + 491-974/His-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 502 AA;

Query Match 100.0%; Score 99; DB 21; Length 552;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 SYDSIKLEPENPPYEAA 18
|||||
151 SYDSIKLEPENPPYEAA 168

|||||

|||||
AAY71388 standard; Protein; 552 AA.

AAY71388;

02-NOV-2000 (first entry)

Rat Nogo A protein fragment used in the construction of mutant Nig-D3.

Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
central nervous system; neoplastic disease; antiproliferative; glioma;
antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
structural plasticity; screening; mutant; mutein.

Rattus sp.

W0200031235 A2.

02-JUN-2000.

05-NOV-1999; 7670-0326100.

06-NOV-1998; 9805-0107446.

(SCHM/) SCHWAB M E.
(CHEN/) CHEN M S.

Schwab ME, Chen MS,

DP WP1; 2000-400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -

XX Example; Page -: 122pp; English.

XX The patent relates to neurite growth inhibitor Nogo which is free of
CC all central nervous system (CNS) myelin material with which it is
CC naturally associated. Nogo proteins and fragments displaying neurite
CC growth inhibitory activity are used in the treatment of neoplastic
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
CC neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
CC diseases. Therapeutics which promote Nogo activity can be used to treat
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
CC acids can be used to inhibit production of Nogo protein to induce
CC regeneration of neurons or to promote structural plasticity of the CNS
CC in disorders where neurite growth, regeneration or maintenance are
CC deficient or desired. The animal models can be used in diagnostic and
CC screening methods for predisposition to disorders and to screen for or
CC test molecules which can treat or prevent disorders or diseases of the
CC CNS. The present sequence is a fragment of rat Nogo A protein shown in
CC AAY71310, which is used in the construction of mutant Nig-D3. Nig-D3
CC is composed of His-tag/77-cag/Nogo-A sequence aa 172-723/His-tag.
CC Nogo A deletion mutants were used for mapping the inhibitory sites of
CC Nogo protein. Major inhibitory region was identified in the
CC Nogo A sequence from amino acids 172-974, particularly amino acids
CC 542-722. In addition, N-terminal region 1-171 was found to be inhibitory
CC to NIH 3T3 fibroblast spreading.
CC Note: The present sequence is not given in the specification but is
CC derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42
CC are referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers.

XX Sequence 552 AA;

Query Match 100.0%; Score 99; DB 21; Length 552;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDSIKLEPENPPYEAA 18
|||||
Nb 452 SYDSIKLEPENPPYEAA 469

|||||
RESULT 8
AAY71394 standard; Protein; 684 AA.

ID AAY71394 standard; Protein; 684 AA.

XX AAY71394;

XX 02-NOV-2000 (first entry)

Rat Nogo A protein fragment used in the construction of mutant Nig-D10.

XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening; mutant; mutein.

XX Rattus sp.

XX W0200031235-A2.

XX 02-JUN-2000.

W0200031235-A2.

02-JUN-2000

05-NOV-1999; 09NOV-US06160

06-NOV-1998; 98US-0107446.

(SCHWAB) SCHWAB M E.
(CHEN/) CHEN M S.

Schwab ME, Chen MS;

WPI; 2000-400052/34

Nogo proteins and nucleic acids useful for treating neuroplastic disorders of the central nervous system and inducing regeneration of neurons.

Example; Page -; 122pp; English

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutic agents which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribosomes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing the fragments of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant Nig-123. Nig-123 is composed of

His-tag/77-Nogo-A sequence aa 172-234 + 232-274/His-tag. Nig-123 deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-274, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from the Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 746 AA;

Query Match 100.0%; Score 99; SE 21; Length 746;

Best Local Similarity 100.0%; Pred No 6e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SYDSIKLEPPNPPIEEA 18
|||||
395 SYDSIKLEPPNPPIEEA 412

NIG 14

N1562

AAV71562 standard; Protein; 803 AA

AAV71562;

02-NOV-2000 (first entry)

Rat Nogo A protein fragment used in the construction of mutant Nig.

XX Rat; neurite growth inhibitor; Nogo A, neural cell, myelin, CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma, meningioma, retinoblastoma;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening; mutant; nucleic.

Rattus sp.

W0200031235-A2.

02-JUN-2000

05-NOV-1999; 09NOV-US06160.

06-NOV-1998; 98US-0107446.

(SCHWAB) SCHWAB M E.
(CHEN/) CHEN M S.

Schwab ME, Chen MS;

WPI; 2000 400052/34.

Nogo proteins and nucleic acids useful for treating neuroplastic disorders of the central nervous system and inducing regeneration of neurons.

Example; Page -; 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutic agents which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribosomes or antisense Nig nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant Nig. The mutant is composed of His-tag/77-Nogo-A sequence aa 172-274/His-tag.

Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo A protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-274, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 803 AA;

Query Match 100.0%; Score 99; SE 21; Length 803;

Best Local Similarity 100.0%; Pred No 6e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSIKLEPPNPPIEEA 18
|||||
DB 452 SYDSIKLEPPNPPIEEA 469

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Comugen Ltd.

protein - protein search, using sw model

January 24, 2003, 11:09:19 : Search time 15 seconds
(without alignments)
115.361 Million cell updates/sec

File: us-09-893-348-19

Effect score: 99

Sequence: 1 SYDSIKLEPENPPPYEBA 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB	ID	Description
1	51.5	2957	2	T33152		hypothetical prote
2	50.5	442	2	S58738		nitrate-binding pr
3	50.5	473	2	A56377		rubber particle cy
4	49.5	458	2	AF2165		bicarbonate transp
5	49.5	1398	2	T25568		hypothetical prote
6	48.5	49.0	307	T40240		dimethylase - flss
7	48.5	49.0	315	T43249		rRNA (adenine-N6,N
8	48.5	90	1	ZNXPLC		zinc finger protei
9	47.5	257	2	F75084		hypothetical prote
10	47.5	591	2	T41531		activator of hsp70
11	47.5	591	2	T51986		hypothetical prote
12	46.5	141	2	P41230		peroxisome prolif
13	46.5	156	2	T18755		hypothetical prote
14	46.5	156	2	P84414		protein B0413.7 [i
15	46.5	330	2	G83853		spore cortex lytic
16	46.5	340	2	T49887		hypothetical prote
17	46.5	475	2	T44264		peroxisome prolif
18	46.5	505	2	A54101		peroxisome prolif
19	46.5	505	2	UC4859		peroxisome prolif
20	46.5	539	2	T21816		hypothetical prote
21	46.5	1113	2	T20100		hypothetical prote
22	45.5	317	2	T00986		yeast pheromone re
23	45.5	400	2	T29121		glycerol-3-phospha
24	45.5	459	2	G83784		hypothetical prote
25	45.5	455	2	A44488		radial spoke prote
26	45.5	475	2	JE0279		peroxisome prolif
27	45.5	477	2	C42214		peroxisome prolif
28	45.5	487	2	JC2495		histamine H1 recep
29	45.5	504	2	JE0280		peroxisome prolif

ALIGNMENTS

RESULT 1

T33152

hypothetical protein T04D1.4 - Caenorhabditis elegans

C.Species: Caenorhabditis elegans

C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C.Accession: T33152

R.Davidson, S.; Wohldmann, P.

submitted to the EMBL Data Library, May 1998

A.Description: The sequence of C. elegans cosmid T04D1.

A.Reference number: 221292

A.Accession: T33152

A.Status: preliminary; translated from GB/EMBL/DDBL

A.Molecule type: DNA

A.Residues: 1-2957 <DAV>

A.Cross-references: EMBL:AF067617; PIRN:AA17569.1; GSPR:GMO0019; GESP:T04D1.4

A.Experimental source: strain Bristol N2; clone T04D1

C.Genetic:

A:Gene: CESP:T04D1.4

A:Map position: 1

A:Introns: 122/3; 293/3; 515/3; 1205/2; 1577/2; 2221/3; 2766/2; 2864/3

Query Match

Best Local Similarity 51.5%; Score 51; DB 2; Length 2957;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 IKLEPENPPYEE 17

DB 464 VKMEPEKSPYQQ 476

RESULT 2

S58738

nitrate-binding protein nrtA precursor, periplasmic [similarity] - Photobacterium lamosum

C.Species: Photobacterium lamosum

C.Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Oct-2000

C.Accession: S58738; S56641; S62124

P.Merchan, F.; Kindle, K.L.; Lama, M.U.; Serra, J.L.; Fernandez, E.

Plant Mol. Biol. 28: 759-766, 1995

A>Title: Cloning and sequencing of the nitrate transport system from the thermophilic, f

cus sp. FCC 794.

A.Reference number: S58738; MUID:95375238; PMID:7647306

A.Accession: S58738

A.Molecule type: DNA

A.Residues: 1-442 <EMR>

A.Cross-references: EMBL:U19598; NID:3114890; PIRN:GA73656.1; PIP:G118393

R.Merchan, F.; Prieto, R.; Kindle, K.L.; Lama, M.U.; Serra, J.L.; Fernandez, E.

Plant Mol. Biol. 27: 1037-1042, 1995

A>Title: Isolation, sequence and expression in Escherichia coli of the nitrate reductase

A.Reference number: S56640; MUID:95284340; PMID:7766873

A.Accession: S56641

A.Status: nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

Residues: 1-67, A: 69, 442 (EMBL)
 Cross-references: EMBL:Z19598

Notes: The nucleotide sequence was submitted to the EMBL Data Library, January 1993
 Accession: AF2165

Keywords: nitrate transport; periplasmic space

Query Match 50.0% Score 50, DP 2, Length 442,
 Best Local Similarity 42.1%, Fred No. 11,
 Matches 7, Conservative 1, Mismatches 6, Indels 0, Gaps 0

2 YNSIKLENNPPPEEA 18
 |||||
 420 EMBL:Z19598:436

Result 3

Query Match 50.0% Score 50, DP 2, Length 442,
 Best Local Similarity 42.1%, Fred No. 11,
 Matches 7, Conservative 1, Mismatches 6, Indels 0, Gaps 0

2 YNSIKLENNPPPEEA 18
 |||||
 420 EMBL:Z19598:436

Query Match 50.0% Score 50, DP 2, Length 473,
 Best Local Similarity 42.1%, Fred No. 12,
 Matches 7, Conservative 1, Mismatches 4, Indels 0, Gaps 0

2 YNSIKLENNPPPEEA 18
 |||||
 435 EMBL:Z19598:436

Query Match 50.0% Score 49, DP 2, Length 458,
 Best Local Similarity 40.0%, Fred No. 16,
 Matches 7, Conservative 1, Mismatches 4, Indels 0, Gaps 0

2 YNSIKLENNPPPEEA 18
 |||||
 444 EMBL:Z19598:436

Query Match 50.0% Score 49, DP 2, Length 458,
 Best Local Similarity 40.0%, Fred No. 16,
 Matches 7, Conservative 1, Mismatches 4, Indels 0, Gaps 0

2 YNSIKLENNPPPEEA 18
 |||||
 444 EMBL:Z19598:436

Result 4

2 YNSIKLENNPPPEEA 17
 |||||
 263 YNLRIPQPKPEPTVE 278

Query Match 49.5% Score 49, DP 2, Length 198,
 Best Local Similarity 43.8%, Fred No. 57,
 Matches 7, Conservative 5, Mismatches 4, Indels 0, Gaps 0

2 YNSIKLENNPPPEEA 17
 |||||
 263 YNLRIPQPKPEPTVE 278

Query Match 49.0% Score 48.5, DP 2, Length 307,
 Best Local Similarity 50.0%, Fred No. 12,
 Matches 8, Conservative 5, Mismatches 0, Indels 3, Gaps 1

2 YNSIKLENNPPPEEA 17
 |||||
 201 VRIKPPPPPIAFEE 216

Query Match 49.0% Score 48.5, DP 2, Length 307,
 Best Local Similarity 50.0%, Fred No. 12,
 Matches 8, Conservative 5, Mismatches 0, Indels 3, Gaps 1

2 YNSIKLENNPPPEEA 17
 |||||
 201 VRIKPPPPPIAFEE 216

Query Match 49.0% Score 48.5, DP 2, Length 307,
 Best Local Similarity 50.0%, Fred No. 12,
 Matches 8, Conservative 5, Mismatches 0, Indels 3, Gaps 1

1. *Primary March* 47.58; *Score* 47; *DB* 2; *Length* 257;
 2. *1st Local* 61.58; *Fund. No.* 17;
 3. *Conservative* 2; *Mismatches* 6; *Gaps* 0;
 4. *Indels* 0;
 5. *2 YDSIKLELEPENNPF* 14

```

;Prox1: Peroxisome proliferator activated receptor gamma 2 - human (fragment)
;Alternate names: peroxisome proliferator activated receptor gamma 1
;Species: Homo sapiens (man)
;Date: 07-Jul-1997 #sequence_18-Jul-1997 #text_change 17-Mar-1999
;Accession: PC4290
;Yanase, T.; Yasuiro, T.; Takitani, K.; Kato, S.; Taniguchi, S.; Takayanagi, E.; Nawata, A.; Biochem. Biophys. Res. Commun. 233, 320-324, 1997
;Title: Differential expression of PPAP gamma 1 and gamma 2 isoforms in human adipose tissue
;Reference number: PC4290; MIM:197280627, PMID:9144532
;Accession: PC4290
;Molecule type: mRNA

```

1141 <YAN>
 Gene reference: inv-pat16
 Experimental source: fat
 Comment: This protein is a nuclear receptor, and plays roles in adipogenesis, adipocyte
 differentially expressed etha-related proteins, etha transforming protein homology
 Query Match 46.5% Score 46; DB 2; Length 141;
 Best Local Similarity 61.6% Pred. No. 13;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 4 SIKLEPPPYEE 17
 100 AAKVFASTFYSH 100
 HIT 13
 906
 Functional protein B0413.7 - Caenorhabditis elegans (fragment)
 Protein: Caenorhabditis elegans
 Date: 16-Oct-1999 #sequence revision 15-Oct-1999 #text_change 15-Oct-1999
 accession: T18765
 Asham, V.
 Submitted to the EMBL Data Library, March 1997
 Reference number: Z19016
 Accession: T18765
 Status: preliminary; translated from GR/EMBL/DBJ
 Molecule type: DNA
 Position: 1-156 <MT>
 Cross reference: EMBL:Z19016, FTH:CA007310.1, CESP:B0413.7
 Protein:
 Name: CESP:B0413.7
 Length: 86/1; 123/1; 149/1
 Query Match 46.5% Score 46; DB 2; Length 156;
 Best Local Similarity 61.6% Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 4 SIKLEPPPP 14
 100 AINEDPPPP 112
 HIT 14
 7418
 Protein B0413.7 (imported) - Caenorhabditis elegans
 Species: Caenorhabditis elegans
 Date: 10-May-2001 #sequence revision 10-May-2001 #text_change 10-May-2001
 Accession: E89418
 Anonymous, The C. elegans Sequencing Consortium.
 Length: 242; 2012 2018, 1998
 Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 Reference number: A5000; MIM:29069613; PMID:9851916
 Note: see website genome.wustl.edu/seq/c_elegans/ and www.sanger.ac.uk/Projects/C_ele
 Notes published online appeared in Science 283, 35, 1999, Science 283, 2103, 1999, and
 Accession: E89418
 Status: preliminary
 Molecule type: DNA
 Position: 1-156 <STO>
 Cross reference: EMBL:Z19016, FTH:CA007310.1, FTH:G4000340, GSTR:G000073, CESP:B0413.7
 Protein:
 Name: B0413.7
 Length: 86/1; 123/1; 149/1
 Map position: 5
 Query Match 46.5% Score 46; DB 2; Length 156;
 Best Local Similarity 61.6% Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 4 SIKLEPPPP 14
 100 AINEDPPPP 112
 HIT 15
 7419

G83853
 spore cortex-lytic enzyme slr (imported) - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans
 C/Date: 01-Dec-2000 #sequence revision 01-Dec-2000 #text_change 15-Jun-2001
 C/Accession: G83853
 P/Takami, H., Nakasone, K., Takaki, Y., Maeno, G., Gaseki, R., Masui, N., Fujii, F., Hirao
 Nucleic Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A/Reference number: A81660, MIM: 201250, PMID: 11058132
 A/Accession: G83853
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-330 <STO>
 A/Cross-references: GB:AF01512; GB:BA000004, MIM:G127400, FTH:BA000004, FTH:G00001
 A/Experimental source: strain C-125
 C/Genetics:
 A/Genes: slrB
 Query Match 46.5% Score 46; DB 2; Length 310;
 Best Local Similarity 60.0% Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 9 PENPPPYEEA 18
 DB 184 PEEPPPYEEA 193
 Search completed: January 24, 2003, 11.11.03
 Job time: 17 secs

GenCore version 5.1.3
Copyright (c) 1994 - 2003 Compugen Ltd

Protein - protein search, using SW model

January 24, 2003, 11:09:44, Search time 18 Seconds
(without alignments)
74,657 Million cell updates/sec

US-09-893-348-19

Effect score: 99
Sequence: 1 SYDSIKLEPPNPPEEA 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Minimum DB seq length: 200000000

Maximum March 08
Listing first 45 summaries

Database: SwissProt_40 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ID	Score	Query	Match	Length	DB	ID	Description
1	99	100.0	1163	1	PTN4_PAT	Q01411	rattus norv
2	95	96.9	1192	1	PTN4_PAT	Q01411	rattus norv
3	48	48.5	90	1	2NRP_LYOVA	P18541	lymphotoxic
4	47	47.5	591	1	STI1_SCHPO	Q05415	schistosom
5	46	46.5	413	1	HXA3_CHICK	Q03353	gallus gall
6	46	46.5	413	1	HXA3_HUMAN	Q03353	gallus gall
7	46	46.5	443	1	HXA3_MOUSE	P02831	mus musculu
8	46	46.5	475	1	PPAT_CRIGR	P57797	cricketulu
9	46	46.5	475	1	PPAT_PATIT	P19052	cricketulu
10	46	46.5	505	1	PPAT_HUMAN	P17231	homo sapien
11	46	46.5	505	1	PPAT_MOUSE	P18924	mus musculu
12	46	46.5	505	1	PPAT_MOUSE	P18924	mus musculu
13	46	46.5	505	1	PPAT_MOUSE	P18924	mus musculu
14	45	45.5	465	1	RSP4_CHIMP	Q01456	chlamydom
15	45	45.5	477	1	PPAT_XENLA	P37234	xenopus lae
16	45	45.5	487	1	HHP1_HUMAN	P15357	homo sapien
17	45	45.5	504	1	PPAT_PIG	P02807	bos scrofa
18	45	45.5	505	1	PPAT_BOVIN	P19491	bos taurus
19	44	44.4	250	1	TRC4_YEAST	P33306	saccharomyc
20	44	44.4	446	1	NPTA_SVYV3	P33452	synchocyst
21	44	44.4	631	1	MX1_MOUSE	P09922	mus musculu
22	44	44.4	801	1	T234_HUMAN	Q15542	homo sapien
23	44	44.4	801	1	BP21_HUMAN	P35443	homo sapien
24	44	44.4	1114	1	TP2M_CABEL	P34534	caenorhabdi
25	44	44.4	1051	1	VGF1_PIRYB	P07930	avian infec
26	43.5	43.9	174	1	CYSC_PIRAB	P66868	pyrococcus
27	43	43.4	265	1	PSA1_TIGER	P32188	tyrannosau
28	43	43.4	304	1	VYCN_CABEL	Q09552	caenorhabdi
29	43	43.4	334	1	PLS_EUSOR	Q05457	eustoma gra
30	43	43.4	337	1	PLS_MALDO	Q05457	eustoma gra
31	43	43.4	348	1	PLS_PETTY	Q07512	petunia hyb
32	43	43.4	349	1	PLS_SOLTU	Q01453	solanum tub
33	43	43.4	440	1	NPTA_ANASP	Q44392	anabesna sp

34	43	43.4	443	1	NPTA_SVYV3	P33306	saccharomyc
35	43	43.4	546	1	VYCN_CABEL	Q09552	caenorhabdi
36	43	43.4	601	1	PLS_EUSOR	Q05457	eustoma gra
37	43	43.4	789	1	PLS_MALDO	Q05457	eustoma gra
38	43	43.4	1787	1	CHD3_CABEL	Q25216	caenorhabdi
39	42	42.4	65	1	VFOR_VACCV	P34516	vacuolabdi
40	42	42.4	172	1	EMEN_MOUSE	P07703	mus musculu
41	42	42.4	464	1	TRIE_METHU	P07703	methanobact
42	42	42.4	489	1	YH98_YEAST	P02825	saccharomyc
43	42	42.4	678	1	PP21_YEAST	P42606	saccharomyc
44	42	42.4	703	1	ML51_HUMAN	Q15234	homo sapien
45	42	42.4	910	1	DDP1_PAT	Q01474	rattus norv

ALIGNMENTS

RESULT 1	PTN4_PAT	STANDARD:	PRT: 1163 AA.
ID	PTN4_PAT	Q01411	rattus norv
AC	Q01411	Q01411	Gapop: 0.000000, Gapext: 0.000000
DT	15-JUN-2002	(Rel. 41, Created)	
DT	15-JUN-2002	(Rel. 41, Last sequence update)	
DT	15-JUN-2002	(Rel. 41, Last annotation update)	
DE	Retraction 4 (Neurite outgrowth inhibitor) (Nogo protein) (Froben)		
DE	(Glut4 vesicle 20 kDa protein).		
GN	RTN4 OR NOGO.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_Taxid=10116;		
PN	[1]		
FT	SEQUENCE FROM N.A. (ISOPROPM 1), AND PARTIAL SEQUENCE.		
RC	STRAIN=Sprague-Dawley; TISSUE=adipocyte.		
RA	MEDLINE=99242816; PubMed=10231557;		
PT	Morris N J, Rose S A, Neven J M, Lane W S, Lienhard G E.		
RT	"Cloning and characterization of a 22 kDa protein from the adipocyte"		
RT	a new member of the reticulon family."		
PL	Biochim. Biophys. Acta 1450:66-76(1994)		
RN	[2]		
PP	SEQUENCE FROM N.A. (ISOPROPM 1; 2 AND 3)		
FX	MEDLINE=20122259; PubMed=1066796;		
PA	Chen M S, Huber A B, Van der Haar M F, Frank M, Schnell L,		
PA	Spillmann A A, Christ F, Schwab M E.		
RT	"Nogo-A is a myelin-associated neurite outgrowth inhibitor and an		
RT	antigen for monoclonal antibody IN-1."		
PL	Nature 403:434-439(2000).		
RN	[3]		
PP	SEQUENCE FROM N.A. (ISOPROPM 2 AND 4).		
PC	STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;		
PA	Ito T, Schwab M E.		
RT	"Cloning of a member of the reticulon gene family in rat: one of two		
RT	minor splice variants."		
PL	Submitted (FPR-1999) to the EMBL/GenBank/DBP1 databases.		
PT	"FUNCTION: Potent neurite outgrowth inhibitor which may also help		
PT	block the regeneration of the nervous central system in adults [by		
PT	similarity].		
CC	"- SUBUNIT: Interacts with Ret-1 and Ret-2 (by similarity).		
CC	"- SUPRACELLULAR LOCATION: Integral membrane protein. Anchored to the		
CC	membrane of the endoplasmic reticulum through a putative		
CC	transmembrane domains (By similarity).		
CC	"- ALTERNATIVE PRODUCTS: 4 isoforms, isoform 1/Meg A/N1 220 250		
CC	(shown here), 2/Meg-B/Froben-N1, 3/Meg-C/VF22 and 4/Froben-M2		
CC	are produced by alternative splicing.		
CC	"- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in retic		
CC	nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are		
CC	present in dorsal root ganglion, sciatic nerve and P17 cells		
CC	after longer exposure. Isoforms 2 and 3 are detected in kidney,		
CC	cartilage, skin, lung and spleen. Isoform 3 is expressed at high		
CC	level in skeletal muscle. In adult animals isoform 1 is expressed		
CC	mainly in the nervous system.		
CC	"- SIMILARITY: CONTAINS 1 RETICULON DOMAIN.		

TISSUE=Testis;
 Sha J.H., Zhou Z.M., Li J.M.;
 Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 [14]
 TOPOLOGY.
 TISSUE=Brain;
 MEDLINE:20122259, PubMed:10667797;
 Grandpre T., Nakamura F., Vartanian T., Stillman S.M.,
 "Identification of the Nogo inhibitor of axon regeneration as a
 Retention protein".
 Nature 403:439-444(2000).
 -1- FUNCTION. Recent neurite outgrowth inhibitor which may also help
 block the regeneration of the nervous central system in adults.
 Isoform 2 reduces the anti-apoptotic activity of Bcl-XL and Bcl-2.
 This is likely consecutive to their change in subcellular
 location, from the mitochondria to the endoplasmic reticulum,
 after binding and sequestration.
 -1- SUBUNIT. Interacts with Bcl-XL and Bcl-2.
 -1- SUBCELLULAR LOCATION. Integral membrane protein. Endoplasmic
 reticulum. Anchored to the membrane of the endoplasmic reticulum
 through 2 putative transmembrane domains.
 -1- ALTERNATIVE PRODUCTS. 4 isoforms. 1/RTN 4A/Nogo-A/RTN-XL (shown
 here), 2/RTN 4B/Nogo-B/RTN-XS/Foocen-M, 3/RTN 4C/Nogo-C/Foocen-
 S and 4; are produced by alternative splicing.
 -1- TISSUE SPECIFICITY. Isoform 1 is specifically expressed in brain
 and testis and weakly in heart and skeletal muscle. Isoform 2 is
 widely expressed excepted for the liver. Isoform 3 is expressed in
 brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 specific.
 -1- SIMILARITY. CONTAINS 1 RETICULON DOMAIN.
 -1- CAUTION. Ref.11 sequence differs from that shown due to
 frameshifts in positions 1149 and 1156.
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 or send an email to license@isb-sib.ch).

EMBL; AJ251383; CAB99248.1; -
 EMBL; AJ251384; CAB99249.1; -
 EMBL; AJ251385; CAB99250.1; -
 EMBL; AB040462; BAB18927.1; -
 EMBL; AB040463; BAB18928.1; -
 EMBL; AF148537; AAG12176.1; -
 EMBL; AF148538; AAG12177.1; -
 EMBL; AF087901; AAG12205.1; -
 EMBL; AF132047; AAD31022.1; -
 EMBL; AF132048; AAD31023.1; -
 EMBL; AB015639; BAA83712.1; -
 EMBL; AF077050; AAD27783.1; -
 EMBL; AF177332; AAG17976.1; -
 EMBL; AB020693; BAA74909.1; -
 EMBL; BC001035; AAH01035.1; -
 EMBL; BC007109; AAH07109.1; -
 EMBL; BC013365; AAH14366.1; -
 EMBL; BC013367; AAH14367.1; -
 EMBL; BC010737; AAH10737.1; -
 EMBL; AF125103; AAD39920.1; -
 EMBL; AF063660; AAG34160.1; -
 EMBL; AF333366; AAK20831.1; -
 GenBank; H04475; ERM4.
 MIM: 604475.
 InterPro: IPR003388; Reticulon.
 Pfam: PF02453; Reticulon_5.
 PROSITE: PS00845; Reticulon_1.
 Endoplasmic reticulum; Alternative splicing; Transmembrane.
 DOMAIN 1 1018 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 1019 1039 POTENTIAL.
 DOMAIN 1040 1133 LUMENAL (POTENTIAL).

FT TRANSMEM 1134 1154
 FT DOMAIN 1155 1192
 FT DOMAIN 1005 1192
 FT DOMAIN 30 47
 FT DOMAIN 143 148
 FT VARSPIC 1 993
 FT VARSPIC 994 1004
 FT VARSPIC 58 289
 FT VARSPIC 186 1004
 FT VARSPIC 107 1004
 FT CONFLICT 135 135
 FT CONFLICT 458 458
 FT CONFLICT 564 564
 FT CONFLICT 684 699
 SQ SEQUENCE 1192 AA; 129930 MW; CDE234RPF11562CA CP764;
 (IN REF. 5)
 Query Match
 Best Local Similarity 85.3%; Score 85; DB 1; Length 1192;
 Matches 15; Conservative 83.3%; Pred. No. 7.6e-05;
 Mismatches 2; Indels 0; Gaps 0;
 QY 1 SYDSIKLEPPNPPYEEA 18
 Db 645 NYESIKLEPPNPPYEEA 662

RESULT 3
 ID ZNFP_LYCVA STANDARD; PRT; 90 AA.
 AC P18541;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Zinc finger protein.
 GN Z.
 OS Lymphocytic choriomeningitis virus (strain Armstrong).
 OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
 OX NCBI_TaxID:11624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:90051057; PubMed:2510401,
 RA Salato M.S., Shimmaye E.M.;
 RT "The completed sequence of lymphocytic choriomeningitis virus reveals
 a unique RNA structure and a gene for a zinc finger protein";
 RL Virology 173:1-10(1989).
 CC -1- FUNCTION: MIGHT BE AN RNA-BINDING PROTEIN WITH A REGULATORY ROLE.
 CC
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DR EMBL; M27693; AAA46268.1; -
 DR PIR; A32592; ZNXPIC.
 DR InterPro: IPR000822; Znf_CCH2.
 DR InterPro: IPR003324; Znf_P1.
 DR PRODOM: PD020016; Znf_P1.1.
 DR PROSITE: PS00028; ZINC_FINGER_CCH2_1; 1.
 KW Zinc-finger; RNA-binding.
 FT ZN_FINGER 32 53
 FT SEQUENCE 90 AA; 10184 MW; D25AF9EC2287E4EA CP664;
 Query Match
 Best Local Similarity 48.5%; Score 49; DB 1; Length 90;
 Matches 8; Conservative 61.5%; Pred. No. 1.4;
 Mismatches 1; Indels 0; Gaps 0;
 QY 5 IKLEPPNPPYEE 17
 Db 78 ISTAPSPPPYEE 90

1-1. SUBCELLULAR LOCATION: Nuclear
1-1. SIMILARITY: REF: N35 TO THE NUCLEAR HORMONE RECEPTOR FAMILY
NRI SUBFAMILY.

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EMBL: U84893; AAB61600.1;

HSSBP; P37231; IFM9.

InterPro: IPR001723; Stahm_receptor

InterPro: IPR001729; Znf_C4steroid

Pfam: PF00104; hormone_rec_1

Pfam: PF00105; zfc_C4_1

PRINTS: PR00399; STROPHOMER

PRINTS: PR00447; STROPHOMER

ProDom: PD000035; Znf_C4steroid.1

SMART: SM00430; HOL1.1

SMART: SM00399; ZNF_C4_1

ProSITE: PS00311; NUCLEAR RECEPTOR_1

Receptor; Transcription regulation. Activator, DNA-binding

Nuclear protein; Zinc-finger, Kolligone family, Phosphorylation

DNA BIND

ZN FING 109 129 C4-TYPE

ZN FING 146 168 C4-TYPE

DOMAIN 288 475 LIGAND BINDING (POTENTIAL)

MOO_PFS 92 92 PHOSPHORYLATION (BY MARK) (BY

SPQWERF 475 AA; 47564 VM; FALYRSCAETTPQET GPCT4;

Very Match 46.5%; Score 46; DB 1; Length 475;

Best Local Similarity 57.1%; Pred. No. 17;

Archae A; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPPNPYPYR 17

75 AIKVEPAPPYSE 88

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

100

PT "Molecular cloning, expression and characterization of human

PT peroxisome proliferator activated receptor gamma 1 and gamma 2.";

PL Submitted (JUL-1996) to the EMBL/GenBank/DBS databases.

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

PC TISSUE=Adipose tissue;

RA Kato S.;

PL Submitted (FEB-1996) to the EMBL/GenBank/DBS databases.

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

PC TISSUE=Bone marrow;

RA MEDLINE=9307072; PubMed=7787419;

RA Greene M.B., Blumberg B., McBride O.W., Yi H.F., Krongauz K.,

RA Kwan K., Hsieh L., Greene G., Nimer S.D.;

PT "Isolation of the human peroxisome proliferator receptor

PT gamma cDNA expressed in hematopoietic cells and chromosomal

PT mapping.";

PL Gene Expr. 4 281-299(1994)

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 1)

PC TISSUE=Placenta,

RA MEDLINE=9406112; PubMed=9156045;

RA Okazawa H., Mori H., Tamai Y., Aoki S., Niki T., Maeyagi J.,

RA Kawanishi M., Kubota T., Shinoda H., Kasuga M.;

PT "Coding mutations are detected in the peroxisome proliferator

PT activated receptor-gamma gene in Japanese patients with lipodipic

PT diabetes.";

PL Diabetes 46 1904-1906(1997).

RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 1)

PC TISSUE=Placenta;

RA MEDLINE=9406159; PubMed=9706492;

RA Jarbe K.G., Jugwood J.D.;

PT "A human peroxisome-proliferator-activated receptor-gamma is

PT activated by inducers of adipogenesis, including 3,3'-diethyl-4,4'-

PT drugs.";

PL Eur. J. Biochem. 239 1-7(1996).

RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)

RA MEDLINE=2037087; PubMed=1092139;

RA Gampe P.T., Montano V.G., Lambert M.H., Miller A.B., Eades R.K.,

RA Milburn W.V., Kilwer S.A., Wilson T.M., Xu H.E.;

PT "Asymmetry in the PPARgamma/RXRalpha crystal structure reveals the

PT molecular basis of heterodimerization among nuclear receptors.";

PL Mol. Cell 5 545-555(2000).

RN [8]

RP VARIANT ALA-12.

RA MEDLINE=9806341; PubMed=9455061;

RA Yen C.-J., Egan P.A., Nigam S., Sliwa E., Brown K.A., Yarnall D.P.;

PT "Molecular scanning of the human peroxisome proliferator activated

PT receptor gamma (hPPAR-gamma) gene in diabetic Caucasians:

PT Identification of a 16023ata PPS-gamma-3 missense mutation.";

PL Biochem. Biophys. Res. Commun. 241 270-274(1997).

RN [9]

RP VARIANT OBESITY GLN-113.

RA MEDLINE=9416646; PubMed=9757170;

RA Ristow M., Muller-Wieland D., Pfeiffer A., Kroe W., Kahn C.R.;

PT "Obesity associated with a mutation in a genetic regulator of

PT adipocyte differentiation.";

PL New Engl. J. Med. 339 953-954(1998)

RN [10]

RP VARIANT ALA-12.

RA MEDLINE=99337654; PubMed=1040729;

RA Harman A., Munzberg H., Butron P., Posing P., Hinney A., Mayer H.,

RA Sigfried W., Heberhard J., Green H.;

PT "Missense variants in the human peroxisome proliferator-activated

PT receptor-gamma 3 gene in lean and obese subjects.";

PL Eur. J. Endocrinol. 141 90-92(1999).

RN [11]

RP VARIANTS COLON CANCER PRO-314 AND HIS-316, AND VARIANT ALA-12.

RA MEDLINE=9722672; PubMed=9339498;

RA Sarraf P., Mueller P., Smith W.M., Wright H.M., Kim J.R.;

-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NRI SUBFAMILY.

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EMBL; AF033103; AAB87480.1; -
EMBL; AF033343; AAB87482.1; -
EMBL; AF033342; AAB87481.1; -
HSSP; P37231; 1F09.
InterPro: IPR000536; Hormone_rec_1ig.
InterPro: IPR001723; Steroid_receptor.
InterPro: IPR001628; Znf_Cstero1d.
Pfam; PF00104; hormone_rec_1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHOMNER.
PRINTS; PR00347; STROIFINGER.
ProDom; PD000635; Znf_Cstero1d; 1.
SMART; SM00430; HOL1; 1.
SMART; SM00389; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; Activator; DNA-binding;
Nuclear protein; Zinc finger; Multigene family; Alternative splicing;
Phosphorylation
ZNF BIND 139 203 NUCLEAR RECEPTOR-TYPE.
DNA BIND 139 150 C4-TYPE.
ZNF BIND 139 150 C4-TYPE.
ZNF BIND 176 154 C4-TYPE.
DOMAIN 318 505 LIGAND BINDING (POTENTIAL).
MOP_PES 112 112 PHOSPHORYLATION (BY MAPK) (BY
SIMILARITY).
VARSPLIC 1 30 MISSING (IN ISOFORM 1).
SEQUENCE 505 AA, 57539 MW, 4183AAE21AA66342 UNQ64;
105 AIKPEPASPYYSE 118

4 SIKLEPPPPPEE 17
: : : : :
105 AIKPEPASPYYSE 118
Query Match 46.58; Score 46; DB 1; Length 505;
Identity 57.14; Field NO. 18;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
4 SIKLEPPPPPEE 17
: : : : :
105 AIKPEPASPYYSE 118
T. MOUSE
P37238; STANDARD; FRT; 505 AA.
01-OCT-1994 (rel. 33, Created)
15-OCT-2001 (rel. 40, Last sequence update)
16-OCT-2001 (rel. 40, Last annotation update)
Peroxisome proliferator activated receptor gamma (PPAR-gamma).
PPARG OR NR1C3.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId:10090;
[1]
SEQUENCE FROM N.A. (ISOFORM 2).
TISSUE=Adipose tissue;
MEDLINE=95011536; PubMed=7926728;
Tontozon P., Hu E., Graves R.A., Budavari A.I., Spiegelman B.M.,
"mPPAR gamma 2: tissue-specific regulator of an adipocyte enhancer";
Genes Dev. 8:1224-1234 (1994).
[2]
SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=BA1B/c; TISSUE=Heart;
MEDLINE=94059089; PubMed=8240342;
Chen F., Law S.W., O'Malley B.W.,
"Identification of two mPPAR related receptors and evidence for the

"Identification of two mPPAR related receptors and evidence for the

RT existence of five subfamily members.";
RL Biochem. Biophys. Res. Commun. 196:671-677(1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=94086482; PubMed=8262913;
RA Zhu Y., Alvares K., Huang Q., Pac M.S., Reddy J.K.;
RT "Cloning of a new member of the peroxisome proliferator-activated
RT receptor gene family from mouse liver";
RL J. Biol. Chem. 268:26817-26820 (1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RX MEDLINE=94316694; PubMed=8041794;
RA Klierer S.A., Forman B.M., Rumberg R., Ong F.S., Polymeyer U.,
RT Mangelsdorf D.J., Umesono K., Evans R.M.,
RT "Differential expression and activation of a family of murine
RL peroxisome proliferator-activated receptors";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7355-7359(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=96249427; PubMed=8647948;
RA Vidal-Puig A., Jimenez-Linan M., Lowell B.B., Hamann A., Hu E.,
RA Spiegelman B., Flier D.S., Moller D.E.,
RT "Regulation of PPAR gamma gene expression by nutrition and obesity in
RT rodents.";
PL J. Clin. Invest. 97:2553-2561(1996).
CC -1- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-CoA
CC OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE
CC OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMEOSTASIS. KEY REGULATOR
CC OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMEOSTASIS.
CC -1- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, 1 AND 2 (SHOWN HERE); ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADIPOSE TISSUE. ALSO
CC FOUND IN LIVER, SKELETAL MUSCLE, HEART, ADRENAL GLAND, STOMACH,
CC KIDNEY AND INTESTINE.
CC -1- DEVELOPMENTAL STAGE: IT APPEARS FIRST AT DAY 13.5 POSTCONCEPTION,
CC AND INCREASES UNTIL BIRTH.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC NRI SUBFAMILY.
CC
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```

VASCULIC      1          30          SIMILARITY)
MUTAGEN       112         112        MISSING (IN ISOFORM 1).
CONFLICT      111         111        S->A INCREASES ACTINOMYCIN ACTIVITY.
SEQUENCE     695 AA, 696-7 MW, P1850AB122EBD3 CPROG4,
               A -> B (IN REF 3).
Query Match   46 %, Score 46, PB 1, Length 605,
Best Local Similarity 57.1%: Pred No. 18;
Matches 9, Conservative 3, Mismatches 3, Indels 0, Gaps 0.

      4 SKLEPNDPPPYEE 17
      ||||| |||||
105 AKVEPASPPYSEE 119

SUBT 14
RSP4 CHLRE STANDARD; PRT: 465 AA.
Q01656;
01-JUN-1993 (Pel 26, Created)
01-JUN-1993 (Pel 26, Last sequence update)
01-OCT-1993 (Pel 27, Last annotation update)
Flagellar radial spoke protein 4.
RSP4.
Chlamydomonas reinhardtii;
Eukaryota; Viridiplantae; Chlorophyta; Chlorellales; Volvocales,
Chlamydomonadales; Chlamydomonas
NCBI Taxonomy;
[!]
SEQUENCE FROM N A
STRAIN: J137,
MEDICAL SOURCE: Patwajitong;
Curry A M., Williams R D., Rosenbaum J L.;
"Sequence analysis reveals homology between two proteins of the
flagellar radial spoke."
Mol Cell Biol 13:1667-1673(1993)
-1- FUNCTION: FLAGELLAR RADIAL SPOKE CONTRIBUTES TO THE PENULTIMATE
OR DIVISION ASK ACTIVITY AND THUS THE PATTERN OF FLAGELLAR BENDING.
THEY CONSIST OF A THIN STALK, WHICH IS ATTACHED TO THE A SUBFIBER
OF THE OUTER DOUBLE MICROTUBULE, AND A FINGER HEAD, WHICH IS
ATTACHED TO THE STALK AND APPEARS TO INTERACT WITH THE
PROTECTIONS FROM THE CENTRAL PAIR OF MICROTUBULES.
-1- SUBUNIT: THE RADIAL SPOKE HEAD IS MADE OF FIVE DIFFERENT
POLYPEPTIDES (RSP1, RSP4, RSP6, RSP9, AND RSP10).
-1- PROPERTIES: LOCATION: CYTOSOL.
-1- SIMILARITY: TO THE FLAGELLAR RADIAL SPOKE PROTEIN 6.

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or send an email to licenses@isb.slb.ch)

EMBL: M87526; AAA3302 1; -
PIR: A44498; A44498.
Flagella.
ProteinPDB 465 AA, 466-9 MW, AC1AFB7C7C9BFA CPROG4,
45.1%, Score 46, DP 1, Length 465,
Std Local Similarity 57.1%; Pred No. 24;
Matches 9, Conservative 3, Mismatches 3, Indels 0, Gaps 0.

      5 IKLEPDNPPPYEEA 18
      ||||| |||||
448 IELKPAPPEEEA 461

SUBT 15
XENLA STANDARD; PRT: 477 AA.
PBAT_XENLA
P37234;
```

```

PP 01-OCT-1994 (Ref: 30, Created)
PT 01-OCT-1994 (Ref: 30, Last sequence update)
PT 16-OCT-2001 (Ref: 40, Last annotation update)
DE Peroxisome proliferator activated receptor gamma (PPAR-gamma) .
SN PPAR-GP NP103.
OS Xenopus laevis (African clawed frog) .
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
CC Amphibia; Batrachia; Anura; Mesobatrachia, Pipridae, Pseudoeurycea;
CC Xenopus; Xenopus.
CC NCBI_TaxID=8355;
RN
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92191267; PubMed=1310391;
RA Dreyer C., Krey G., Keller H., Givel F., Helftenbein G., Wahl W.;
RT "Control of the peroxisomal beta-oxidation pathway by a novel family
RL of nuclear hormone receptors."
RL Cell 68:879-887(1992) .
RN
RN CHARACTERIZATION.
RP MEDLINE=9410015; PubMed=8274443;
RX Krey G., Keller H., Mahfoudi A., Medin J., Ozato K., Dreyer C.,
PA Wahl W.;
PA "Xenopus peroxisome proliferator activated receptors: genomic
RT organization, response element recognition, heterodimer formation
RT with retinoid X receptor and activation by fatty acids."
RT Steroid Biochem M-1 Bio- 47 65-73(1993) .
RT FUNCTION: PROMOTER THAT BIND PEROXISOME PROLIFERATORS SUCH AS
RT DIFFERENT DRUGS AND FATTY ACIDS. SHRE ACTIVATED BY A LIGAND,
RT THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-CoA
RT OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE
RT PEROXISOMAL BETA OXIDATION PATHWAY OF FATTY ACIDS. KEY REGULATOR
RT OF ACTIVATED DIFFERENTIATION AND TISSUE HOMEOSTASIS.
CC SHIMUNT, HETERODIMER WITH THE RETINOID X RECEPTOR.
CC 1- SPECIFICALLY LOCATED IN THE NUCLEAR.
CC 1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN ADIPOSE TISSUE AND KIDNEY
CC 1- DEVELOPMENTAL STAGE: ADULT.
CC 1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC 1- NRI SUBFAMILY.
CC
CC THIS SWISS-PROT entry is annotated. It is provided through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ebi.ac.uk/ebih/faq.html
CC or send an email to license@ebi-sib.ch)
CC
CC EMBL, M84163, AAA4937.1, .
CC PIR: C42214; C42214.
CC DR HSSP: P37231; 1PM9.
CC DR TRANSFAC: T01264, .
CC DR InterPro: IPP000536; Hormone_rec_1lg.
CC DR InterPro: IPP001723; Steroid_receptor.
CC DR InterPro: IPP001628; ZnF_C4steroid.
CC Pfam: PF00104; hormone_rec; 1.
CC Pfam: PF00105; zf-C4; 1.
CC DR PRINTS: PR00398; STRPSPRMNER.
CC DR PRINTS: PR00047; STROIDPFINGER.
CC DR PROSITE: PR00035; ZnF_C4steroid; 1.
CC DR SMART: SMO0430; HOL1; 1.
CC DR SMART: SMO0399; ZnF_C4; 1.
CC DR ProSite: PS00031; NUCFAP_PPAPPRC; 1.
CC KeyWord: Transcription regulation, activator, DNA binding;
CC Nuclear protein; Zinc finger, Multigene family, Phosphorylation.
FT DN_BIND 113 177 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 113 133 C4-TYPE.
FT ZN_FING 150 172 C4-TYPE.
FT DOMAIN 293 477 LIGAND-BINDING (POTENTIAL) .
FT MOD_RES 87 87 PHOSPHORYLATION (BY MAPK) (BY
FT SIMILARITY)
SO SEQUENCE 477 AA; 5405 MW; 160F7A9D1C67246 CRC64;

```

1. *Correct similarity*: 57.18; *Prod.*: No. 24;
2. *Correct*: 4; *Correct-val*: 20; *Mismatches*: 1; *Misses*: 4.

4; Mismatches

3; indels

0; Gaps

EXHIBIT

[illegible]

Figure 1. Schematic diagram of the experimental setup. The subject is seated in a chair and views the target through a video camera. The target is a light source that is controlled by a computer. The subject's hand is positioned at the target. The distance between the subject and the target is 100 cm. The target is a light source that is controlled by a computer. The subject's hand is positioned at the target. The distance between the subject and the target is 100 cm.

Completed: January 24, 2008, 11:10:51
 User: j. j. j.

[illegible]

Thesis (1993). Biochemistry and Molecular Biology,
University of Basque Country.

[2] SEQUENCE FROM N A
STRAIN=OH-1-P-CL1;
Merchan F ;

[3] Submitted (JAN-1993) to the EMBL/GenBank/CCDB databases

[4] SEQUENCE FROM N A
STRAIN=OH-1-P-CL1;
Merchan F ;

[5] Submitted (JAN-1996) to the EMBL/GenBank/CCDB databases

SEQUENCE FROM N A
STRAIN=OH-1-P-CL1;
Merchan F ; Kinda K L, Llana M J, Serra J L, Fernandez E ;
"Isolation, sequence and expression in *Escherichia coli* of the nitrate
reductase gene from the filamentous, thermophilic cyanobacterium
Phormidium laticolor." ;
Plant Mol Biol 27:1037-1042 (1995).

[4] SEQUENCE FROM N A
STRAIN=OH-1-P-CL1;
Fernandez E ;

[5] Submitted (JAN-1996) to the EMBL/GenBank/CCDB databases

SEQUENCE FROM N A
STRAIN=OH-1-P-CL1;
MEDLINE=20375239, PubMed-7647306,
Merchan F ; Kinda K L, Llana M J, Serra J L, Fernandez E ;
"Cloning and sequencing of the nitrate transport system from the
thermophilic, filamentous cyanobacterium *Phormidium laticolor*;
Comparative analysis with the homologous system from *Thiobacillus
ferrooxidans* and *Syntherisma* sp. NCC 7940." ;
Plant Mol Biol 28:759-766 (1995).

EMBL: Z19598; CAA79666.1 ;
SEQUENCE 442 AA, 47719 MW, 76A0FDB409535F8 CRC64;

Query March 50.58, Score 50, DB 2, Length 442;
Best local similarity 47.18; Pred. No. 14;
Matches 8, Conservative 3, Mismatches 6, Indels 0, Gaps 0,

2 YDSIKLEPNPPYEAA 18
:|||||
420 FDGVKDPENPSAYLSA 436

420 FDGVKDPENPSAYLSA 436

778
CUT 5
340778 PRELIMINARY; PRT; 473 AA.

040778: PRELIMINARY; PRT; 473 AA.

01-AUG-1998 (TRENDEL) 07, Created
01-AUG-1998 (TRENDEL) 07, Last sequence update)

01-MAR-2002 (TRENDEL) 20, Last annotation update)
Allene oxide synthase (EC 4.2.1.22) (Fatty acyl-CoA oxidase) (FPO)
RPP30.

Parthenium argentatum.

Euphorbia, Vitaceae, Stereophylla, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicot,
Asterales, Asteridae II, Asterales; Asteraceae; Asteroideae;
Helianthaceae; Parthenium

NCBI_Taxid:39035.

[1] SEQUENCE FROM N A, AND PARTIAL SEQUENCE
STRAIN=LINE 11901; TISSUE=STEM BAPV;

MEDLINE=20375239, PubMed-7647306,
Pan Z, Durr F, Weyck-Pelchardt D, Gardner H W, Camara R,

Conzel K, Backhaus P A ;
"The major protein of guayule rubber particles is a cytochrome P450
characterization based on cDNA cloning and spectroscopic analysis of
the solubilized enzyme and its reaction products." ;
J. Biol. Chem 270:8490-8494 (1995).

[2] SEQUENCE FROM N A, AND PARTIAL SEQUENCE
STRAIN=LINE 11901; TISSUE=STEM BAPV;

MEDLINE=20375239, PubMed-7647306,
Pan Z, Camara R, Gardner H W, Backhaus P A ;
"Aspirin inhibition and acetylation of the plant cytochrome P450,

RT allene oxide synthase, resembles that of animal prostaglandin

PL J. Biol. Chem. 273:18139-18145 (1998)

CC -1- FUNCTION: IS INVOLVED IN THE BIOSYNTHESIS OF JASMONIC ACID, A
GROWTH REGULATOR THAT IS IMPLICATED ALSO AS A SIGNALING MOLECULE
IN PLANT DEFENSE ACTS ON A NUMBER OF UNSATURATED FATTY ACID
HYDROPEROXIDES, FORMING THE CORRESPONDING ALLYL OXIDES (BY
SIMILARITY)

CC -1- CATALYTIC ACTIVITY (EC:1.1.1.142) (118) HYDROPEROXYOXYGENASE-
(O₂), (11,14)-TRIENIN = (3O)- (11,13)-DIEN-3-OL + H₂O.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

DE EMBL: X78166; CAA55025.1 ;
DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

DE EMBL: X78166; CAA55025.1 ;

Q95U02; Q9Y7V3;
 01-MAY-2000 (TReMBLrel. 13, Created)
 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6'-N', N'-ADENOSYL (PRNA) dimethyltransferase) (18S RNA dimethylase).
 DIM1 OR SPBC336.02.
 Schizosaccharomyces pombe (Fission yeast).
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 NCBI_TaxID=4896;
 (1)
 SEQUENCE FROM N.A.
 Housen I., Demotte D., Lafontaine D., Vandenhaute J.;
 "Cloning and comparative analysis of the SPD1 gene from
 Schizosaccharomyces pombe";
 Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 (2)
 SEQUENCE FROM N.A.
 STRAIN=972;
 Borzym K., Beck A., Reinhardt R., McDougall R.C., Rajadream M.A.,
 Barrell B.G.;
 Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 -1- FUNCTION: SPECIFICALLY DIMETHYLATES TWO ADJACENT ADENOSINES IN THE
 LOOP OF A CONSERVED HAIRPIN NEAR THE 3'-END OF 18S RNA IN THE 40S
 PARTICLE.
 -1- SIMILARITY: BELONGS TO THE RNA ADENINE N-6-METHYLTRANSFERASE
 FAMILY.
 EMBL; 268293; CAA92585.1; -;
 EMBL; AL121815; CAB58154.1; -;
 InterPro: IPR001737; RNA_A_dimeth.
 InterPro: IPR000051; SAM_Bind.
 Pfam: PF00398; RrnaAD.1.
 TIGRfam: TIGR00755; KsgA.1.
 PROSITE: PS01131; RNA_A_DIMETH.1.
 MRNA Processing; Transferase; Methyltransferase.
 DRAIN 208 211
 CONFLICT 170 170 S -> P (IN REF. 1).
 CONFLICT 290 292 TEF -> QS (IN REF. 1).
 CONFLICT 298 298 A -> P (IN REF. 1).
 CONFLICT 304 307 VFPA -> RSFWMGGDGVFH (IN REF. 1).
 SEQUENCE 307 AA; 34678 MW; E2F453EB190894A CRC64;
 Query Match 49.0%; Score 48.5; DB 3; Length 307;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 8; Conservative 5; Mismatches 0; Indels 3; Gaps 1;
 5 IKLEPNPP---YFE 17
 ::::|||||
 201 VRIEKNPPPLAFEE 216
 ::::|||||
 (1)
 TO
 Q9DCT0 PRELIMINARY; PRT; 158 AA.
 Q9DCT0;
 01-JUN-2001 (TReMBLrel. 17, Created)
 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 0610010012Pik Protein.
 0610010012Pik.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 (1)
 SEQUENCE FROM N.A.
 STRAIN=C57BL/6J; TISSUE=KIDNEY;
 MEDLINE=21085660; PubMed=11217851;
 Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Komio H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Miyasaka H., Konjo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.W., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barb G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
 RA Brownstein M.T., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima U., Mazzarelli U., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Williams L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaj H., Kohlsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 DR EMBL; AK002512; EMB22153.1; -;
 DR MGD; MGI:1913310; 0610010012Pik.
 SQ SEQUENCE 158 AA; 16764 MW; 9122F577DF49D2B4 CRC64;
 Query Match 48.5%; Score 48; DB 11; Length 158;
 Best Local Similarity 77.8%; Pred. No. 9.9;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 7 LEPNPPY 15
 ::::|||||
 DB 1 MNPENPPY 9

RESULT 11
 ID Q9UES1 PRELIMINARY; PRT; 125 AA.
 AC Q9UES1;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Hypothetical 14.3 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Barlow I.K.-P., Boguski M.S., Touchman J., Spencer F.;
 RT "Full-insert sequence of mapped XREF EST.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF091078; AAC72947.1; -;
 DR InterPro; IPR001737; RNA_A_dimeth.
 DR Pfam; PF00398; RrnaAD.1.
 KW Hypothetical protein.
 SQ SEQUENCE 125 AA; 14275 MW; 9E2E91518577BD01 CRC64;
 Query Match 47.5%; Score 47; DB 4; Length 125;
 Best Local Similarity 60.0%; Pred. No. 11;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 5 IKLEPNPP 14
 ::::|||||
 DB 19 VRIEKNPP 28

RESULT 12
 ID Q76025 PRELIMINARY; PRT; 157 AA.
 AC Q76025;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

COMPILED HEADABLE FORM:
MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,200
 FILING DATE: 07 JUN 1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: REITER, STEPHEN E.
 REGISTRATION NUMBER: 31,192
 FIRM: EPOCH, RONALD M. 341 971
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619 546-9192
 TELEFAX: 619 546-9192
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MULTIPLE TYPE: protein
 484 200 2

Query Match 46.5% Score 46; DB 3; Length 475;
 Best Local Similarity 57.1% Pred. No. 30;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

4 SIKLEPPPPYEE 17
 :|||:|||||
 75 AIKVEPASPYYSE 88

GENERAL INFORMATION:
 APPLICANT: Scanlan, Thomas S.
 APPLICANT: Baxter, John D.
 APPLICANT: Fletcher, Robert J.
 APPLICANT: Wagner, Richard L.
 APPLICANT: Kushner, Peter J.
 APPLICANT: Kushner, Peter J.

Query Match 46.5% Score 46; DB 3; Length 475;
 Best Local Similarity 57.1% Pred. No. 30;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

4 SIKLEPPPPYEE 17
 :|||:|||||
 75 AIKVEPASPYYSE 88

GENERAL INFORMATION:
 APPLICANT: Scanlan, Thomas S.
 APPLICANT: Baxter, John D.
 APPLICANT: Fletcher, Robert J.
 APPLICANT: Wagner, Richard L.
 APPLICANT: Kushner, Peter J.
 APPLICANT: Kushner, Peter J.

APPLICANT: Apiletti, James W
 APPLICANT: West, Brian
 TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
 TITLE OF INVENTION: Binding Domains
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESS: Cooley Godward
 STREET: Five Palo Alto Square, 3000 El Camino Real
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/764,870
 FILING DATE: 13-DEC-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/004,540
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,543
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,606
 FILING DATE: 14-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Nakamura, Jackie N
 REGISTRATION NUMBER: 35,966
 REFERENCE/AGENT NUMBER: 341 100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)843-5000
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 484 200 10

Query Match 46.5% Score 46; DB 4; Length 475;
 Best Local Similarity 57.1% Pred. No. 33
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 SIKLEPPPPYEE 17
 :|||:|||||
 Db 75 AIKVEPASPYYSE 88

RESULT 5
 US-08-980-115-10
 Sequence 10, Application US/08/980,115
 Patent No. 6266622
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Thomas S.
 APPLICANT: Baxter, John D.
 APPLICANT: Fletcher, Robert J.
 APPLICANT: Wagner, Richard L.
 APPLICANT: Kushner, Peter J.
 APPLICANT: Apiletti, James W.
 APPLICANT: West, Brian L.
 APPLICANT: Shlau, Andrew K.
 TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
 FILE REFERENCE: USAL-246/0205
 CURRENT APPLICATION NUMBER: US/08/980,115
 CURRENT FILING DATE: 1997-11-26
 EARLIER APPLICATION NUMBERS: 08/764,870
 EARLIER FILING DATE: 1996-12-13

```

NAME: 110b1e, Jack W.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594 5321
TELEFAX: (908) 594-4720
INFORMATION FOR SEQUENCING:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids

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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2
34-128 142 2

Query Match 46.5% Score 46, DB 4, Length 477,
Best Local Similarity 57.1%, Filed No. 32,
Matches 8, Conservative 3, Mismatches 3, Gaps 0

4 SIKLEPPNPPYEE 17
|||||
77 ALKVEPASPYYSE 93

HIT 9
34-128 142 4
Sequence 4, Application US/00128142
Patent No. 6294559
GENERAL INFORMATION:

APPLICANT: Smith, Roy C.
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH
PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA AND GABA

NUMBER OF SEQUENCES: 4
ADDRESS: Jack L. Tibble
STREET: 126 E. Lincoln Ave., P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065 0907

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Power Macintosh 7500/100
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,142
FILING DATE: 03 Aug 1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/P44,007
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Tibble, Jack L.
REGISTRATION NUMBER: 12,633
REFERENCE/DOCKET NUMBER: <unknown>
TELEPHONE/DOCKET INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4.
39 128 142 4

Query Match 46.5% Score 46, DB 4, Length 505,
Best Local Similarity 57.1%, Filed No. 32,
Matches 8, Conservative 3, Mismatches 3, Gaps 0

4 SIKLEPPNPPYEE 17
|||||
105 ALKVEPASPYYSE 118

HIT 10
39 128 142 6
Sequence 6, Application US/0014247A

Patent No. 6365361
GENERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OF SCREENING AGONIST AND ANTAGONIST TO PPAR
FILE REFERENCE: TANIGUCHI-6
CURRENT APPLICATION NUMBER: US/02/514,247A
CURRENT FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: PCT/JP99/03734
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent version 3.0
SEQ ID NO: 6
LENGTH: 506
TYPE: PRT
ORGANISM: Homo sapiens
US-09-514-247A-6

Query Match 46.5% Score 46, DB 4, Length 506,
Best Local Similarity 57.1%, Filed No. 32,
Matches 8, Conservative 3, Mismatches 3, Gaps 0

QY 4 SIKLEPPNPPYEE 17
|||||
DB 105 ALKVEPASPYYSE 118

RESULT 11
US-08-861-269-5
Sequence 5, Application US/08861269
Patent No. 5817494
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purni
TITLE OF INVENTION: PEPTIDIN CONJUGATION PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/04/861,269
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0302 US
TELEPHONE/DOCKET INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: 397581
CLONE: GenBank

Query Match 44.4% Score 44, DB 2, Length 250,
Best Local Similarity 80.0%, Pred. No. 30,
Matches 8, Conservative 0, Mismatches 2, Indels 0, Gaps 0

6 KLEPENPPY 15
15 KLEVENPPY 24

OUT 12

09-134-596-5
Sequence 5, Application US/09134596
Patent No. 592218

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Corley, Neil C.

APPLICANT: Lal, Preethi

APPLICANT: Shah, Purni

TITLE OF INVENTION: HEPATITIN CONJUGATION PROTEINS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/134,596

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/841,009

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF 0302 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOFOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: 397581

CLONE: GenBank

09-134-596-5

Query Match 44.4% Score 44, DB 2, Length 250,
Best Local Similarity 80.0%, Pred. No. 30,
Matches 8, Conservative 0, Mismatches 2, Indels 0, Gaps 0

6 KLEPENPPY 15
15 KLEVENPPY 24

OUT 13

09-293-273-5
Sequence 5, Application US/09293273
Patent No. 607111

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Corley, Neil C.

APPLICANT: Lal, Preethi

APPLICANT: Shah, Purni

TITLE OF INVENTION: HEPATITIN CONJUGATION PROTEINS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/293,273

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/134,596

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0302 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOFOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: 397581

CLONE: GenBank

US-09-293-273-5

Query Match 44.4% Score 44, DB 3, Length 250,
Best Local Similarity 80.0%, Pred. No. 30,
Matches 8, Conservative 0, Mismatches 2, Indels 0, Gaps 0

6 KLEPENPPY 15
15 KLEVENPPY 24

RESULT 14

US-08-379-556A-4

Sequence 4, Application US/08379556A

Patent No. 5859329

GENERAL INFORMATION:

APPLICANT: HOISON, TIMOTHY A.

APPLICANT: KEAM, LISA A.

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOL

TITLE OF INVENTION: SYNTHASE ENZYMES AND USES THEREFORE

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: SCULLY SCOTT MURPHY & PRESSER

STREET: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY

STATE: NEW YORK

COUNTRY: USA

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Polysome #1.0, Version #1.30

REPORT APPLICATION DATA:

APPLICATION NUMBER: US/08/179,556A

EXPIRATION DATE: 22 MAR 1995

CLASSIFICATION: 439

APPLICANT: FRANK, A. A.

NAME: FRANK, A. A.

REGISTRATION NUMBER: 31,346

REGISTRATION DATE: 1992

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REGISTRATION DATE: 1992

REGISTRATION NUMBER: 31,346

Score 43; DB 2; Length 241;
Pred. No. 40;
Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 70.0%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 9 PENPPPYEA 18
Db 162 PKNPPSYEA 171

Search completed January 24, 2003, 11:12:10
Job time: 16 secs

Score 43; DB 2; Length 347;

GenCore version 5.1.3
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Protein Protein search, using sw model

January 24, 2003, 11:10.33 / Search time 10 seconds
(without alignments)

36.321 Million cell updates/sec

US-09-893-348-19

Effect score: 1 SYDSIKLEPPENPPYEBA 18

Sequence: 1 SYDSIKLEPPENPPYEBA 18

Aligned: 122236 seqs, 20178551 residues

Number of hits satisfying chosen parameters: 122236

Minimum DB seq length: 0

Minimum PR seq length: 200000000

Minimum Match 100%

Listing first 45 summaries

Published Applications AA:

- 1: /cgn2_6/ptodara/2/pubppa/US08 NEW PUB pep:*
- 2: /cgn2_6/ptodara/2/pubppa/PCT_NEW PUB pep:*
- 3: /cgn2_6/ptodara/2/pubppa/US06 NEW PUB pep:*
- 4: /cgn2_6/ptodara/2/pubppa/US06 PUB COMB pep:*
- 5: /cgn2_6/ptodara/2/pubppa/US07 NEW PUB pep:*
- 6: /cgn2_6/ptodara/2/pubppa/US07 PUB COMB pep:*
- 7: /cgn2_6/ptodara/2/pubppa/PCUS PUB COMB pep:*
- 8: /cgn2_6/ptodara/2/pubppa/US09 NEW PUB pep:*
- 9: /cgn2_6/ptodara/2/pubppa/US09 PUB COMB pep:*
- 10: /cgn2_6/ptodara/2/pubppa/US10 NEW PUB pep:*
- 11: /cgn2_6/ptodara/2/pubppa/US10 PUB COMB pep:*
- 12: /cgn2_6/ptodara/2/pubppa/US06 NEW PUB pep:*
- 13: /cgn2_6/ptodara/2/pubppa/US06 PUB COMB pep:*
- 14: /cgn2_6/ptodara/2/pubppa/US06 PUB COMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score	Query	Match	Length	ID	Description
99	100.0	18	10	US-09-893-348-19	Sequence 19, Appl
99	100.0	1163	10	US-09-893-348-18	Sequence 18, Appl
85	85.9	1192	10	US-09-889-386-2	Sequence 6, Appl
85	85.9	1192	10	US-09-758-140-6	Sequence 6, Appl
85	85.9	1192	10	US-09-893-348-23	Sequence 23, Appl
85	85.9	1192	10	US-09-893-348-23	Sequence 54, Appl
50	50.5	405	10	US-09-884-260A-54	Sequence 2, Appl
46	46.5	475	12	US-10-142-373-2	Sequence 27, Appl
46	46.5	478	10	US-09-765-111A-27	Sequence 27, Appl
46	46.5	505	10	US-09-765-111A-16	Sequence 16, Appl
46	46.5	506	12	US-10-109-886-6	Sequence 6, Appl
46	46.5	688	9	US-09-931-007A-1	Sequence 1, Appl
46	46.5	777	10	US-09-765-111A-23	Sequence 23, Appl
46	46.5	811	10	US-09-765-111A-4	Sequence 4, Appl
46	46.5	840	10	US-09-765-111A-6	Sequence 39748, A
45	45.5	874	10	US-09-864-761-39748	Sequence 297, App
43	43.4	158	10	US-09-841-132-297	Sequence 411, App
43	43.4	609	10	US-09-841-132-431	Sequence 411, App

20	43	43.4	789	9	US-09-712-363-24	Sequence 24, App
21	43	43.4	912	9	US-09-865-960-2	Sequence 2, Appl
22	43	43.4	928	10	US-09-993-170-58	Sequence 58, Appl
23	42	42.4	73	9	US-10-001-887-94	Sequence 94, Appl
24	42	42.4	624	10	US-09-925-297-738	Sequence 738, App
25	42	42.4	913	10	US-09-223-490-4	Sequence 4, Appl
26	41	41.4	128	10	US-09-925-299-85	Sequence 492, App
27	41	41.4	429	10	US-09-864-761-34248	Sequence 6, Appl
28	40.5	40.9	2665	10	US-09-908-670-1	Sequence 34248, A
29	40	40.4	311	10	US-09-925-302-666	Sequence 1, Appl
30	40	40.4	313	10	US-09-925-302-666	Sequence 666, Appl
31	40	40.4	684	10	US-09-765-298A-18	Sequence 18, Appl
32	40	40.4	731	9	US-10-086-464-8	Sequence 8, Appl
33	39.5	39.9	402	10	US-09-925-301-984	Sequence 984, App
34	39	39.4	59	10	US-09-764-877-1169	Sequence 1169, App
35	39	39.4	63	10	US-09-864-761-36982	Sequence 36982, A
36	39	39.4	99	10	US-09-925-300-1634	Sequence 1634, App
37	39	39.4	119	9	US-09-862-209A-24	Sequence 24, Appl
38	39	39.4	119	9	US-10-086-623-24	Sequence 24, Appl
39	39	39.4	146	9	US-10-174-590-376	Sequence 376, App
40	39	39.4	146	9	US-10-176-758-376	Sequence 376, App
41	39	39.4	146	9	US-10-175-737-376	Sequence 376, App
42	39	39.4	146	12	US-10-052-556-376	Sequence 376, App
43	39	39.4	200	9	US-10-107-868-16	Sequence 16, Appl
44	39	39.4	200	12	US-10-107-829-16	Sequence 16, Appl
45	39	39.4	200	12	US-10-107-907-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-893-348-19
Sequence 19, Application US/09893348
Patent No. US20020072493A1
GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michael
APPLICANT: COHEN, Irwin R.
APPLICANT: BESERMAN, Pierre
APPLICANT: MOSONIGO, Alton
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVEOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
FILE REFERENCE: EIS-SCHWARTZ-CA
CURRENT APPLICATION NUMBER: US/09/893,348
PRIOR FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: PCT/US98/14715
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ. ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ. ID NO 19
LENGTH: 18
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-893-348-19

Query Match 100.0%; Score 99; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

QY 1 SYDSIKLEPPENPPYEBA 18
Db 1 SYDSIKLEPPENPPYEBA 18

RESULT 2
US-09-893-348-18
Sequence 18, Application US/09893348

[illegible]

```

Patent No. US20020012965A1
GENERAL INFORMATION:
APPLICANT: Strittmatter, Stephen M.
FILE OF INVENTION: US 09/200,129.6A; Entry: WIPO PCT Int. Cl. 6 A. 01 Growth
FILE REFERENCE: 44574-5073-US
CURRENT APPLICATION NUMBER: US 09/768,140
CURRENT FILING DATE: 2001-01-12
PRIORITY APPLICATION NUMBER: US 60/175,707
PRIORITY FILING DATE: 2000-01-12
PRIORITY APPLICATION NUMBER: US 60/297,966
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 60/236,378
PRIORITY FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
LENGTH: 1192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-758-140-6

Query Match      85.9%; Score 85; DB 10; Length 1192;
Best Local Similarity 83.3%; Pred. No. 0.00027;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 SYDSIKLEPPNPPEEA 18
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DB      645 NYESIKHEPNPPPEEA 662

RESULT 5
US-09-893-348-23
3-49-23, Application US/09090348
Patent No. US20020072493A1
GENERAL INFORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michael
APPLICANT: COHEN, Irvin P
APPLICANT: BESEMAN, Pierre
APPLICANT: MOSCONESO, Alon
APPLICANT: MOLEME, Gila
TITLE OF INVENTION: ACTIVATED T CELLS, NEUTROS SYSTEM SPECIFIC ANTIGENS AND THEIR USES
FILE REFERENCE: EIS-SCHWARTZ:2A
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT FILING DATE: 2001-07-29
PRIORITY APPLICATION NUMBER: US 09/314,161
PRIORITY FILING DATE: 1999-05-19
PRIORITY APPLICATION NUMBER: US 09/218,277
PRIORITY FILING DATE: 1998-12-22
PRIORITY APPLICATION NUMBER: EPO/0398/14715
PRIORITY FILING DATE: 1999-07-21
PRIORITY APPLICATION NUMBER: IL 124500
PRIORITY FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent In version 3.1
SEQ ID NO 23
LENGTH: 1192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-893-348-23

Query Match      85.9%; Score 85; DB 10; Length 1192;
Best Local Similarity 83.3%; Pred. No. 0.00027;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 SYDSIKLEPPNPPEEA 18
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DB      645 NYESIKHEPNPPPEEA 662

RESULT 6
US-09-972-599A-6
Sequence 6, Application US/09972599A
Patent No. US2002007295A1

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GENERAL INFORMATION:
 APPLICANT: STRITTMATTER, STEPHEN M
 TITLE OF INVENTION: NOVA RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
 FILE REFERENCE: C077 CIP US
 CURRENT APPLICATION NUMBER: US/09/072,590A
 CURRENT FILING DATE: 2001-10-06
 PRIOR APPLICATION NUMBER: PCT/US01/01041
 PRIOR FILING DATE: 2001-01-12
 PRIOR APPLICATION NUMBER: 09/758,140
 PRIOR FILING DATE: 2001-01-12
 PRIOR APPLICATION NUMBER: 60/236,379
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/207,366
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/175,707
 PRIOR FILING DATE: 2000-01-12
 NUMBER OF SEQ ID NOS: 57
 SOFTWARE: Patent Ver 2.1
 SEQ ID NO: 6
 LENGTH: 1192
 TYPE: PRT
 ORGANISM: Homo sapiens
 09-972-599A-6

Query Match 85.9%; Score 85; DB 10; Length 1192;
 Best Local Similarity 83.3%; Pred. No. 0.00027;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 SIKLEPPPPYEEA 18
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 645 NYEKIEPPPPYEEA 662

UT 7
 09-884-260A-54
 Applicant: Alan Brash
 GENERAL INFORMATION:
 APPLICANT: Nathalie Tijer
 TITLE OF INVENTION: MYOGENESIS AND USES THEREOF
 FILE REFERENCE: 06027 000272
 CURRENT APPLICATION NUMBER: US/03/984,260A
 CURRENT FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: 09/537,357
 PRIOR FILING DATE: 2000-03-29
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 54
 LENGTH: 405
 TYPE: PRT
 ORGANISM: Guayule
 09-884-260A-54

Query Match 50.5%; Score 50; DB 10; Length 405;
 Best Local Similarity 47.1%; Pred. No. 6.5;
 Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

2 YDSIKLEPPPPYEEA 18
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 180 YFSIKLEPPPPYEEA 196

UT 8
 0-142 373-2
 Applicant: Evans, Ronald
 GENERAL INFORMATION:
 APPLICANT: Evans, Ronald
 TITLE OF INVENTION: METHODS OF PEROXISOME PROLIFERATOR ACTIVATED
 TITLE OF INVENTION: RECEPTOR GAMMA,

TITLE OF INVENTION: AND METHODS FOR THE USE THEREOF
 FILE REFERENCE: SAK1480-2
 CURRENT APPLICATION NUMBER: US/10/142,373
 CURRENT FILING DATE: 2002-05-08
 PRIOR APPLICATION NUMBER: US/09/788,070
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: US 09/045,302
 PRIOR FILING DATE: 1999-02-22
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Patent version 3.0
 SEQ ID NO: 2
 LENGTH: 475
 TYPE: PRT
 ORGANISM: Mus Musculus
 US 10 142 373-2

Query Match 46.5%; Score 46; DB 12; Length 475;
 Best Local Similarity 57.1%; Pred. No. 28;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPPPPYEE 17
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RESULT 9
 US-09-765-111A-27
 Sequence 27, Application US/09765111A
 Patent No. US0020106796A1
 GENERAL INFORMATION:
 APPLICANT: Fletcher, Jonathan A.
 APPLICANT: Kroell, Todd G.
 TITLE OF INVENTION: FAX8-SPARAGMA NUCLEIC ACID MOLECULES
 FILE REFERENCE: B0801/7196/ESP/MAT
 CURRENT APPLICATION NUMBER: US/09/765,111A
 CURRENT FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: US 60/177,109
 PRIOR FILING DATE: 2000-01-20
 PRIOR APPLICATION NUMBER: US 60/225,079
 PRIOR FILING DATE: 2000-09-14
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 27
 LENGTH: 478
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-09-765-111A-27

Query Match 46.5%; Score 46; DB 10; Length 478;
 Best Local Similarity 57.1%; Pred. No. 28;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPPPPYEE 17
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 77 AIKVEPPASPPYSE 90

RESULT 10
 US-09-765-111A-16
 Sequence 16, Application US/09765111A
 Patent No. US0020106796A1
 GENERAL INFORMATION:
 APPLICANT: Fletcher, Jonathan A.
 APPLICANT: Kroell, Todd G.
 TITLE OF INVENTION: FAX8-SPARAGMA NUCLEIC ACID MOLECULES
 FILE REFERENCE: B0801/7196/ESP/MAT
 CURRENT APPLICATION NUMBER: US/09/765,111A
 CURRENT FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: US 60/177,109
 PRIOR FILING DATE: 2000-01-20
 PRIOR APPLICATION NUMBER: US 60/225,079

09-765-111A-23

Query Match	46.5%	Score 46;	DB 10;	Length 811;
Best Local Similarity	57.1%	Pred No 49;		

Best Local Similarity 57.1%; Pred No 49;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPPPYEE 17

411 AIKVEPASPPYSE 424

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REPORT NO. US20020106796A1
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kroll, Todd G.

TITLE OF INVENTION: AND

CURRENT APPLICATION NUMBER: US/03/765,11A

PRIOR APPLICATION NUMBER: US 60/177,109

PRIOR APPLICATION NUMBER: US

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FBI WINDOWS VERSION 3.0
EQ ID NO 4

LENGTH: 840
TYPE: PRT

ORGANISM: *Homo sapiens*
09-765-111A-4

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Set	Items	Description
S1	2483	NOGO
S2	143	S1 AND NEUR?
S3	2141	S1 AND NERV?
S4	51	S1 AND CENTRAL(W)NERVOUS(W)SYSTEM
S5	361	ED (unique items)
S6	4	S1 AND SPINAL(W)CORD
S7		AU='EISENBACH-SCHWARTZ MICHAL'
S8		AU='HAUBEN, EHUD'
S9		AU='HAUBEN, E.'
S10	9	AU='HAUBEN E.'
S11	1	AU='HAUBEN EHUI'
S12	5	AU='HAUBEN E.'
S13	14	AU='COHEN, IRUN R'
S14	11	AU='COHEN IRUN R'
S15	80	AU='COHEN I R.'
S16	36	AU='COHEN I.R.'
S17		AU='BESERMAN PIERRE'
S18	4	AU='MOALEM G'
S19	2	AU='MOALEM G.'
S20	1	AU='MOALEM GILA'
S21		AU='MOALEM, GILA'
S22		NOGO AND S7 OR S8 OR S9 OR S10 OR S11 OR S12 OR S13 OR S14 OR S15 OR S16 OR S17 OR S18 OR S19 OR S20 OR S21)
S23	1	ED (unique items)
S24	46	NOGO AND SPINAL(W)CORD
S25	35	ED (unique items)
S26	16	S25 AND DEGENEFAT?
S27	66	S25 AND REGENEFAT?
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 DIALOG
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 1/24/2003



	Type	Hits	Search Text	DBs
1	BRS	14	EISENBACH-SCHWARTZ-M	USPAT; US-PGPUB; EPO; JPO; DERWENT
2	BRS	16	EISENBACH-SCHWARTZ-MICHAL	USPAT; US-PGPUB; EPO; JPO; DERWENT
3	BRS	3	HAUBEN-EHUD	USPAT; US-PGPUB; EPO; JPO; DERWENT
4	BRS	55	COHEN-IRUN-R	USPAT; US-PGPUB; EPO; JPO; DERWENT
5	BRS	5	BESERMAN-PIERRE	USPAT; US-PGPUB; EPO; JPO; DERWENT
6	BRS	12	BESERMAN	USPAT; US-PGPUB; EPO; JPO; DERWENT
7	BRS	2	MOSONEGO-ALON	USPAT; US-PGPUB; EPO; JPO; DERWENT
8	BRS	2	MOALEM-GILA	USPAT; US-PGPUB; EPO; JPO; DERWENT
9	BRS	266	Nogo	USPAT; US-PGPUB; EPO; JPO; DERWENT
10	BRS	9	Nogo and neuro\$	USPAT; US-PGPUB; EPO; JPO; DERWENT
11	BRS	12	p472	USPAT; US-PGPUB; EPO; JPO; DERWENT
12	BRS	10	Nogo and central adj nervous adj system	USPAT; US-PGPUB; EPO; JPO; DERWENT
13	BRS	6	nogo and spinal adj cord	USPAT; US-PGPUB; EPO; JPO; DERWENT

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